

Barb O'Bryan

140693 = Art

SEARCH REQUEST FORM

142410 = Text

Requestor's

Name: My Phan Team ¹⁴⁹³³ Serial Number: 09/380,447
Date: 12/17/04 Phone: 272-0810 Art Unit: 1639
Mail box: REM C2A05

2104

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Mrs. O'Bryan,

Please search claim 1 →

and the following

limitations:

- 1) The major coat protein is a M13 filamentous phage (SEQ ID No. 2)
- 2) Its variants are as follows:

Details

- 3) The heterologous poly peptide is an antibody that bind to a target, which is *erb2*.
- 4) The heterologous poly peptide is link to the major coat protein by a linking peptide of SEQ ID No. 110

Thanks 11

S. Sidhu G. Weiss J. Wells - Mod. of coat protein

STAFF USE ONLY

Date completed: 1-12-05Searcher: PERBTerminal time: 25 60Elapsed time: 20 30

CPU time: _____

Total time: _____

Number of Searches: 4

Number of Databases: _____

Search Site

 STIC

Vendors

 IG Suite CM-1 218/300 STN Pre-S Dialog

Type of Search

 N.A. Sequence APS A.A. Sequence Geninfo Structure SDC Bibliographic DARC/Questel

=> fil reg; d que 110
FILE 'REGISTRY' ENTERED AT 09:39:33 ON 12 JAN 2005
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 10 JAN 2005 HIGHEST RN 811411-12-8
DICTIONARY FILE UPDATES: 10 JAN 2005 HIGHEST RN 811411-12-8

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:

<http://www.cas.org/ONLINE/DBSS/registryss.html>

L10 13 SEA FILE=REGISTRY ABB=ON [AD] [EK] [GS] [DE] [DK] [PF] [AS] [KR] [AD]A
[FY] [NE] [SA]L[QE] [AD] [SI] [AI]T[EN] [YL] [IF] [GF] [YL] [AL] [WG] [AT] [MV] [VY] VVIVGATIGIKLFFKFTSKAS/SQSFP

=> d rn cn sql kwic nte lc 110 1-13

L10 ANSWER 1 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 799856-67-0 REGISTRY - *Use Registry # to match sequence to citation (beginning on pg 6)*
CN 7: PN: WO2004101608 SEQID: 7 unclaimed protein (9CI) (CA INDEX NAME)
SQL 77

SEQ 1 SGTAMADPNR FRGKDLAGSP GGGGGGAEG DDPAKAAFNS LQASATEYIG
===== =====
51 YAWAMVVVIV GATIGIKLKF KFTSKAS
===== =====

HITS AT: 28-77

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 2 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 685484-38-2 REGISTRY
CN GenBank AAT27365 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAT27365 (Translated from: GenBank AY598820)
SQL 73

SEQ 1 MKKSLVLKAS VAVATLVPML SFAAEGDDPA KAAFNSLQAS ATEYIGYAWA
===== =====
51 MVVIVGATI GIKLFFKFTS KAS
===== =====

HITS AT: 24-73

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L10 ANSWER 3 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 480506-95-4 REGISTRY

CN GenBank CAA23861 (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank CAA23861 (Translated from: GenBank V00604)

SQL 73

SEQ 1 MKKSLVLKAS VAVATLVPML SFAAEGDDPA KAAFNSLQAS ATEYIGYAWA

===== ===== =====

51 MVVVIVGATI GIKLFKKFTS KAS

===== ===== =====

HITS AT: 24-73

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L10 ANSWER 4 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 460400-92-4 REGISTRY

CN L-Serine, L-alanyl-L- α -glutamylglycyl-L- α -aspartyl-L- α -aspartyl-L-prolyl-L-alanyl-L-lysyl-L-alanyl-L-alanyl-L-phenylalanyl-L-asparaginyl-L-seryl-L-leucyl-L-glutaminyl-L-alanyl-L-seryl-L-alanyl-L-threonyl-L- α -glutamyl-L-tyrosyl-L-isoleucylglycyl-L-tyrosyl-L-alanyl-L-tryptophyl-L-alanyl-L-methionyl-L-valyl-L-valyl-L-valyl-L-isoleucyl-L-valylglycyl-L-alanyl-L-threonyl-L-isoleucylglycyl-L-isoleucyl-L-lysyl-L-leucyl-L-phenylalanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-threonyl-L-seryl-L-lysyl-L-alanyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3: PN: WO02072780 SEQID: 10 unclaimed protein

SQL 50

SEQ 1 AEGDDPAKAA FNSLQASATE YIGYAWAMVV VIVGATIGIK LFKKFTSKAS

===== ===== ===== ===== =====

HITS AT: 1-50

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L10 ANSWER 5 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 405053-51-2 REGISTRY

CN L-Serine, L-alanyl-L- α -glutamylglycyl-L- α -aspartyl-L- α -aspartyl-L-prolyl-L-alanyl-L-lysyl-L-alanyl-L-alanyl-L-phenylalanyl-L-asparaginyl-L-seryl-L-leucyl-L-glutaminyl-L-alanyl-L-seryl-L-alanyl-L-threonyl-L- α -glutamyl-L-tyrosyl-L-isoleucylglycyl-L-tyrosyl-L-alanyl-L-tryptophyl-L-alanyl-L-methionyl-L-valyl-L-valyl-L-valyl-L-isoleucyl-L-valylglycyl-L-alanyl-L-threonyl-L-isoleucylglycyl-L-isoleucyl-L-lysyl-L-leucyl-L-phenylalanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-threonyl-L-seryl-L-lysyl-L-alanyl- (9CI) (CA INDEX NAME)

SQL 50

SEQ 1 AEGDDPAKAA FNSLQASATE YIGYAWAMVV VIVGATIGIK LFKKFTSKAS

===== ===== ===== ===== =====

HITS AT: 1-50

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L10 ANSWER 6 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 346502-45-2 REGISTRY

CN 21: PN: US6251865 SEQID: 21 unclaimed protein (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1: PN: WO0187323 PAGE: 39 unclaimed sequence

SQL 77

SEQ 1 SGTAMADPNR FRGKDLAGSP GGGSGGGAEG DDPAKAAFNS LQASATEYIG

===== ===== =====

51 YAWAMVVVIV GATIGIKLFK KFTSKAS

HITS AT: 28-77

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L10 ANSWER 7 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 316203-10-8 REGISTRY
CN Protein A (synthetic *Staphylococcus aureus* clone pAlg-816 precursor N-terminal fragment) fusion protein with immunoglobulin, anti-(Z-DNA) (mouse single-chain) fusion protein with protein (coliphage M13 gene III coat C-terminal fragment) (9CI) (CA INDEX NAME)
SQL 364

SEQ 301 KLEIKHHHHH GSGTAEGDDP AKAAFNSLQA SATEYIGYAW AMVVVIVGAT
===== ===== ===== =====
351 IGIKLFKKFT SKAS
===== =====

HITS AT: 315-364
LC STN Files: CA, CAPLUS

L10 ANSWER 8 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 151033-87-3 REGISTRY
CN (1-6)-(9-21)-Phosphatase, alkaline (*Escherichia coli* precursor reduced) fusion protein with trypsin inhibitor (cattle pancreas basic reduced) fusion protein with protein (coliphage M13 coat) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN (1-6)-(9-21)-Phosphatase, alkaline (*Escherichia coli* precursor reduced) fusion protein with trypsin inhibitor (ox pancreas basic reduced) fusion protein with protein (coliphage M13 coat)
OTHER NAMES:
CN (1-6)-(9-21)-Phosphatase, alkaline (*Escherichia coli* precursor reduced) fusion protein with trypsin inhibitor (ox pancreas basic reduced) fusion protein with protein (bacteriophage M13 coat)
SQL 127

SEQ 51 TFVYGGCRAK RNNFKSAEDC MRTCGGAAEG DDPAKAAFNS LQASATEYIG
===== ===== =====
101 YAWAMVVVIV GATIGIKLFK KFTSKAS
===== ===== =====

HITS AT: 78-127
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L10 ANSWER 9 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN
RN 144999-51-9 REGISTRY
CN Trypsin inhibitor (cattle pancreas basic reduced), (58 \rightarrow 1')-protein with protein (coliphage M13 coat) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Trypsin inhibitor (ox pancreas basic reduced), (58 \rightarrow 1')-protein with protein (coliphage M13 coat)
OTHER NAMES:
CN Trypsin inhibitor (ox pancreas basic reduced), (58 \rightarrow 1')-protein with protein (bacteriophage M13 coat)
SQL 108

SEQ 51 CMRTCGGAAE GDDPAKAAFN SLQASATEYI GYAWAMVVVI VGATIGIKLF
===== ===== =====
101 KKFTSKAS
=====

HITS AT: 59-108
LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 10 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 144999-50-8 REGISTRY
CN 1-21-Phosphatase, alkaline (Escherichia coli precursor reduced),
(21 \rightarrow 1')-protein with trypsin inhibitor (cattle pancreas basic
reduced) (58 \rightarrow 1')-protein with protein (coliphage M13 coat) (9CI)
(CA INDEX NAME)

OTHER CA INDEX NAMES:

CN 1-21-Phosphatase, alkaline (Escherichia coli precursor reduced),
(21 \rightarrow 1')-protein with trypsin inhibitor (ox pancreas basic reduced)
(58 \rightarrow 1')-protein with protein (coliphage M13 coat)

OTHER NAMES:

CN 1-21-Phosphatase, alkaline (Escherichia coli precursor reduced),
(21 \rightarrow 1')-protein with trypsin inhibitor (ox pancreas basic reduced)
(58 \rightarrow 1')-protein with protein (bacteriophage M13 coat)

SQL 129

SEQ 51 CQTFVYGGCR AKRNNFKSAE DCMRTCGGAA EGDDPAKAAF NSLQASATEY
= =====
101 IGYAWAMVVV IVGATIGIKL.FKKFTSKAS
=====

HITS AT: 80-129

LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 11 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 114013-90-0 REGISTRY

CN 1-142-Kinase (phosphorylating), ribulo- (Salmonella typhimurium reduced)
142-glycine-, (142 \rightarrow 11')-protein with 11-73-protein (coliphage M13
gene 8) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1-142-Kinase (phosphorylating), ribulo- (Salmonella typhimurium reduced)
142-glycine-, (142 \rightarrow 11')-protein with 11-73-protein (bacteriophage
M13 gene 8)

SQL 205

SEQ 151 MLSFAAEGDD PAKAAFNSLQ ASATEYIGYA WAMVVIVGA TIGIKLFKKF
=====
201 TSKAS
=====

HITS AT: 156-205

LC STN Files: CA, CAPLUS

L10 ANSWER 12 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 104364-70-7 REGISTRY

CN Protein (coliphage M13 coat) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2: PN: WO0006717 SEQID: 2 unclaimed protein

CN Protein (bacteriophage M13 coat)

SQL 50

SEQ 1 AEGDDPAKAA FNSLQASATE YIGYAWAMVV VIVGATIGIK LFKKFTSKAS
=====

HITS AT: 1-50

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, TOXCENTER

L10 ANSWER 13 OF 13 REGISTRY COPYRIGHT 2005 ACS on STN

RN 76560-64-0 REGISTRY

CN Protein (coliphage M13 coat precursor) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Protein (bacteriophage M13 coat precursor)

SQL 73

SEQ 1 MKKSLVLKAS VAVATLVPML SFAAEGDDPA KAAFNSLQAS ATEYIGYAWA

51 MVVVIVGATI GIKLFFKFTS KAS

HITS AT: 24-73

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

=> => fil capl; s 110
FILE 'CAPLUS' ENTERED AT 09:40:26 ON 12 JAN 2005
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*Registry file
answer set
crossed into bibliographic
files to get citations*

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FILE COVERS 1907 - 12 Jan 2005 VOL 142 ISS 3
FILE LAST UPDATED: 10 Jan 2005 (20050110/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L15 12 L10

=> fil uspatf toxcenter; s 110
FILE 'USPATFULL' ENTERED AT 09:40:36 ON 12 JAN 2005
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L16 9 L10

=> dup rem 115,116
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FILE 'TOXCENTER' ENTERED AT 09:40:40 ON 12 JAN 2005
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PROCESSING COMPLETED FOR L15
PROCESSING COMPLETED FOR L16

L17 13 DUP REM L15 L16 (8 DUPLICATES REMOVED)
ANSWERS '1-12' FROM FILE CAPLUS
ANSWER '13' FROM FILE USPATFULL

Copyright GenCore version 5.1.6 (c) 1993 - 2005 CompuGen Ltd.

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: January 12, 2005, 10:43:39 ; Search time 28 Seconds

142.110 Million cell updates/sec
(without alignments)

OM protein - protein search, using SW model
Run on: January 12, 2005, 11:00:20 ; Search time 97.5 Seconds
(without alignments)
222,332 Million cell updates/sec

Perfect score: 304
Sequence: 1 AWEENIDSAPEAGDDAKAA. VIVGATIGIKLFPKKFTSKAS 66
Scoring table: BLOSUM62
Gapop 10.0 , **Gapext** 0.1

Title: SEQ010-THEN-SEQ2
Perfect score: 304
Sequence: I AWEENIDSAFAPAEQDDPAKAA:..... VIVGATATIGIKLIFKKFV
Scoring table: BLOSUM62
Gapop 10.0 , **Gapext** 0.1
Searched: 1608061 seqs, 361289386 residues

Searched: 478139 seqs, 66318000 residues
Total number of hits satisfying chosen parameters: 478139

Total number of bits satisfying chosen parameters: 1608061
Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum DB seq length: 2000000000

Maximum Match listing first

Database : Issued Patents AA:*

```
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being analyzed and is derived by analysis of the total score distribution.

Recall No.	Score	Query	Match	Length	DB	ID	Description
1	248	81.6	50	1	US-08-133-011-17		Sequence 17, APP
2	248	81.6	50	1	US-08-322-730A-17		Sequence 17, APP
3	248	81.6	50	1	US-08-387-874-17		Sequence 17, APP
4	248	81.6	50	2	US-08-383-619-17		Sequence 17, APP
5	248	81.6	50	3	US-08-907-739-17		Sequence 17, APP
6	248	81.6	50	4	US-09-729-597-17		Sequence 17, APP
7	248	81.6	50	5	PCT-US930-08364-17		Sequence 17, APP
8	248	81.6	77	3	US-08-825-852-21		Sequence 21, APP

SUMMARIES						
Result No.	Score	% Match	Length	DB	ID	Description
10	248	81.6	77	4	US-09-723-890-21	Sequence 21, Appl
11	248	81.6	77	4	US-09-723-901-21	Sequence 21, Appl
12	248	81.6	77	4	US-09-723-547-21	Sequence 21, Appl
13	248	81.6	77	4	US-09-724-127-21	Sequence 21, Appl
14	248	81.6	77	4	US-09-723-931-21	Sequence 21, Appl
15	248	81.6	77	4	US-09-723-873-21	Sequence 21, Appl
16	248	81.6	77	4	US-09-724-114-21	Sequence 21, Appl
17	248	81.6	77	4	US-09-723-913-21	Sequence 21, Appl
18	248	81.6	77	4	US-09-723-912-21	Sequence 21, Appl
19	248	81.6	77	4	US-09-724-095-21	Sequence 21, Appl
20	248	81.6	77	4	US-09-724-157-21	Sequence 21, Appl
21	248	81.6	77	4	US-09-724-052-21	Sequence 21, Appl
22	248	81.6	77	4	US-09-724-065-21	Sequence 21, Appl
23	244	80.3	73	4	US-09-495-880A-9	Sequence 9, Appl
24	244	80.3	73	4	US-09-495-880A-24	Sequence 24, Appl
25	244	80.3	73	4	US-09-495-880A-40	Sequence 40, Appl
26	234	77.0	72	4	US-09-866-073A-17	Sequence 17, Appl
27	71.4	23.5	625	4	US-09-538-073A-1064	Sequence 1064, Appl

GenCore version 5.1.6
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using sw model

Om protein - protein search, using sw model

Run on: January 12, 2005, 10:11:18 ; Search time 126 Seconds
Perfect score: 304
Sequence: 1 AWEENIDSAAPAEQDDPAKAA.....VIVGATIGIKLFLKFKFTSKAS 60
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: SEQ110-THEN-SEQ2
1825181 seqs, 575314646 residues

Run on: January 12, 2005, 10:42:14 ; Search time 24.5 Seconds
Perfect score: 304
Sequence: 1 AWEENIDSAAPAEQDDPAKAA.....VIVGATIGIKLFLKFKFTSKAS 60
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Total number of hits satisfying chosen parameters: 1825181
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Description

Result No. Score Query Match Length DB ID Description

Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	244	80.3	73	1	COAB_BPFD	P03617 bacteriophaga
2	243	79.9	50	2	Q9TQ9	bacteriophaga
3	238	78.3	50	1	COAB_BPQJ2	P03618 bacteriophaga
4	206	67.8	65	2	Q8211	Q38211 bacteriophaga
5	173.7	57.1	74	1	COAB_BP1F1	P03619 bacteriophaga
6	97	31.9	84	1	COAB_BP1F2	P15416 bacteriophaga
7	93	30.6	53	2	Q9TQ9B	Q9TQ9B bacteriophaga
8	90	29.6	82	1	COAB_BP1KE	P03620 bacteriophaga
9	75.2	24.7	183	2	Q9P4D4	Q9F4D1 burkholderi
10	75.1	24.7	1070	2	Q15X9	Q6i5x9 oryza sativ
11	73.5	24.2	476	2	Q9A3A6	Q9A3A6 caulobacter
12	72.8	23.9	351	1	YEE5_THRAC	Q9h187 thermoplasma
13	71.7	23.6	535	2	Q5577	Q5577 synochocyst
14	71.4	23.5	253	2	Q9C514	Q8C514 mub musculu
15	71.4	23.5	504	2	Q60786	Q60786 mus musculu
16	71.4	23.5	540	2	Q811S7	Q811S7 mus musculu
17	71.4	23.5	653	1	MLA1_HUMAN	P33908 homo sapien
18	71.4	23.5	1031	2	Q9BFT4	Q8eff4 shewanella
19	71.1	23.4	228	2	Q73038	Q73u88 mycobacteri
20	71.1	23.4	228	2	Q9A6080	Q9A6080 mycobacteri
21	70.7	23.3	2167	2	Q92EKS	Q92EKS listeria in
22	70.3	23.1	400	2	Q99114	Q89i14 bradyrhizob
23	70.2	23.1	436	2	Q9Y2A4	Q89z4 bacteroides
24	70.2	23.1	499	2	Q9JP16	Q73p16 treponema
25	70.2	23.1	499	2	AWEENIDSA	Aasi1474 treponema
26	69.9	23.0	700	2	Q9N1474	Q7ns1 mycobacteri
27	69.5	22.9	236	2	Q99ED0	Q89ed0 bradyrhizob
28	69.4	22.8	523	2	Q9VBS1	Q7vbs1 prochlorococ
29	69.4	22.8	1285	2	Q9Y132	Q6y132 lactuca sat
30	69.4	22.8	1285	2	Q9Q72578	Qaq72578 lactuca sat
31	69.3	22.8	710	2	Q9C6N0	Q6c6n0 yarrowia li